

10036328 Results

SEQ ID NO: 2

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	6238	100.0	1210	5	AAU98551	Aau98551 Novel hum
2	6187.5	99.2	1211	6	ABR61471	Abr61471 Human sec
3	5695.5	91.3	1138	5	AAU98553	Aau98553 Novel hum
4	3841.5	61.6	733	5	AAU98552	Aau98552 Novel hum
5	3807.5	61.0	735	7	ADE34400	Ade34400 Human G-p
6	3361.5	53.9	714	6	ABG73643	Abg73643 Human G-p
7	3315.5	53.2	662	5	AAU98554	Aau98554 Novel hum
8	2866.5	46.0	2570	4	ABG06375	Abg06375 Novel hum
9	2509	40.2	486	5	ABP52435	Abp52435 Human G p
10	1957.5	31.4	395	6	ABR61470	Abr61470 Human sec
11	1313.5	21.1	1014	6	ABJ38840	Abj38840 Human G-p
12	1313.5	21.1	1014	6	ABJ38832	Abj38832 Human epi
13	1313.5	21.1	1014	6	ABP81971	Abp81971 Human G p
14	1313.5	21.1	1014	6	ABR61472	Abr61472 Human sec
15	1313.5	21.1	1014	7	ADB80456	Adb80456 Ovarian c
16	1313.5	21.1	1038	2	AAW36903	Aaw36903 Human epi
17	1313	21.0	1013	3	AAB01247	Aab01247 Human HE6

RESULT 1

AAU98551

ID AAU98551 standard; protein; 1210 AA.

XX

AC AAU98551;

XX

DT 26-AUG-2002 (first entry)

XX

DE Novel human GPCR, 7TM protein #1.

XX

KW Human; G protein-coupled receptor; GPCR; 7TM protein;

KW physiological disorder; behavioural disorder; cosmetic; nutraceutical;

KW seven transmembrane protein; receptor.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Misc-difference 1201

FT /note= "Encoded by YTT"

XX

PN WO200236633-A2.

XX

PD 10-MAY-2002.

XX

PF 29-OCT-2001; 2001WO-US050938.

XX

PR 30-OCT-2000; 2000US-0244285P.

XX

PA (LEXI-) LEXICON GENETICS INC.

XX

PI Hu Y, Zambrowicz B, Nepomnichy B;

XX

DR WPI; 2002-490002/52.

DR

N-PSDB; ABK85471.

XX

PT New human G protein-coupled receptor polynucleotide useful for

PT therapeutic, diagnostic and pharmacogenomic applications, and for

PT identifying compounds that modulate gene expression or gene product

PT

activity.

XX

PS Claim 2; Page 73-76; 86pp; English.

XX

CC The present invention relates to novel human G protein-coupled receptor

CC (GPCR) proteins referred to as 7TM proteins, and the polynucleotide

CC sequences encoding them. The novel 7TM proteins have multiple
CC transmembrane regions. The polynucleotide and polypeptide sequences of
CC the invention can be used in the treatment of physiological or
CC behavioural disorders, and/or in cosmetic or nutraceutical applications.
CC The present sequence represents a human 7TM protein of the invention

XX

SQ Sequence 1210 AA;

Query Match 100.0%; Score 6238; DB 5; Length 1210;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1210; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MTSSNTQPLLMTSWNIPTAEGSQFP	ISTTINVPTS	NEMETETLHLVPGPLSTFTASQTGL	60					
Db	1	MTSSNTQPLLMTSWNIPTAEGSQFP	ISTTINVPTS	NEMETETLHLVPGPLSTFTASQTGL	60					
Qy	61	VSKDVMAMSSIPMSGILPNHGLSEN	PSLSTSLRAITSTLADV	KHTFEKMTTSVTPGTTLP	120					
Db	61	VSKDVMAMSSIPMSGILPNHGLSEN	PSLSTSLRAITSTLADV	KHTFEKMTTSVTPGTTLP	120					
Qy	121	SILSGATSGSVISKSPILTWLLSSL	PSGSPPATVSNAPHVMTS	SSTVEVSKSTFLTSDMIS	180					
Db	121	SILSGATSGSVISKSPILTWLLSSL	PSGSPPATVSNAPHVMTS	SSTVEVSKSTFLTSDMIS	180					
Qy	181	AHPFTNLTTLP	SATMSTILTR	TIPTPTLGGITTGFPTSLPMSINVTDDIVYISTHPEASS	240					
Db	181	AHPFTNLTTLP	SATMSTILTR	TIPTPTLGGITTGFPTSLPMSINVTDDIVYISTHPEASS	240					
Qy	241	RTTITANPRTVSH	PSSFSRK	TMSPTTDDHTLSVGAMPLPSSTITSSWNRIPTASSPSTLI	300					
Db	241	RTTITANPRTVSH	PSSFSRK	TMSPTTDDHTLSVGAMPLPSSTITSSWNRIPTASSPSTLI	300					
Qy	301	IPKPTLDSLLNIMTTT	STVPGAS	FPLISTGV	TYPF	TATVSSPISSFFETT	WLDSTPS	FLS	360	
Db	301	IPKPTLDSLLNIMTTT	STVPGAS	FPLISTGV	TYPF	TATVSSPISSFFETT	WLDSTPS	FLS	360	
Qy	361	TEASTSPTATKSTV	SFYNVEM	SFSVFVEE	PRIPIT	SVINEFTENSLNSIFQNSEFSLATL	420			
Db	361	TEASTSPTATKSTV	SFYNVEM	SFSVFVEE	PRIPIT	SVINEFTENSLNSIFQNSEFSLATL	420			
Qy	421	ETQIKSRDISEEEM	VMDRAILE	QREGQEMATISYVPYSCVCQV	IIKASSSLASSEL	MRKI	480			
Db	421	ETQIKSRDISEEEM	VMDRAILE	QREGQEMATISYVPYSCVCQV	IIKASSSLASSEL	MRKI	480			
Qy	481	KSKIHGNFTHGNFT	QDQLTLLV	NCEHVA	VKKLEPGNCKADE	TASKYKGT	YKWL	LTNP	TET	540
Db	481	KSKIHGNFTHGNFT	QDQLTLLV	NCEHVA	VKKLEPGNCKADE	TASKYKGT	YKWL	LTNP	TET	540
Qy	541	AQTRCIKNEDGNAT	RFC	SISINTGKSQWEKPKFKQCKLLQEL	PKIVDLANITISDENPE	600				
Db	541	AQTRCIKNEDGNAT	RFC	SISINTGKSQWEKPKFKQCKLLQEL	PKIVDLANITISDENPE	600				
Qy	601	DVAEHILN	LINESPALGKEET	KIIVSKISDISQCDEISMNLTHV	MLQIINVVLEKQNN	SA	660			
Db	601	DVAEHILN	LINESPALGKEET	KIIVSKISDISQCDEISMNLTHV	MLQIINVVLEKQNN	SA	660			
Qy	661	SDLHEISNEILRI	I	IERPGHKMEFSGQIANLAVAGLALAVLRGDHTFDGMAFSIHSYEEGP	720					
Db	661	SDLHEISNEILRI	I	IERPGHKMEFSGQIANLAVAGLALAVLRGDHTFDGMAFSIHSYEEGP	720					
Qy	721	DPDIFLGNVPVGG	ILASIYLPKSLTERIPLSNLQ	PILFNFFGQTS	LFKTKNVTKALT	TYV	780			
Db	721	DPDIFLGNVPVGG	ILASIYLPKSLTERIPLSNLQ	PILFNFFGQTS	LFKTKNVTKALT	TYV	780			
Qy	781	VSASISDMFIQN	LADPVVITLQHIGGNQNYGQVHCAF	WDFENNNGLGWNSSGCKVKETN	840					
Db	781	VSASISDMFIQN	LADPVVITLQHIGGNQNYGQVHCAF	WDFENNNGLGWNSSGCKVKETN	840					
Qy	841	VNYTICQCDHL	THFGVLM	DLRSRSTVDSVNEQILALITYTGCGISSIFLG	VAVVTYIA	AFHK	900			
Db	841	VNYTICQCDHL	THFGVLM	DLRSRSTVDSVNEQILALITYTGCGISSIFLG	VAVVTYIA	AFHK	900			

Qy 901 LRKDYPKILINLCTALLMLNLVFLINSWLSSFQKVGVCITAAVALHYFLLVSFTWMGLE 960
 |||||
 Db 901 LRKDYPKILINLCTALLMLNLVFLINSWLSSFQKVGVCITAAVALHYFLLVSFTWMGLE 960

Qy 961 AVHMYLALVKVFNIYIPNYILKFCLVGWGIPAIMVAITVSVKKDLYGTLSPTTPFCWIKD 1020
 |||||
 Db 961 AVHMYLALVKVFNIYIPNYILKFCLVGWGIPAIMVAITVSVKKDLYGTLSPTTPFCWIKD 1020

Qy 1021 DSIFYISVVAYFCLIFLMNLSMFCTVLVQLNSVKSQIQKTRRKMLHDLKGTMSLTFLLG 1080
 |||||
 Db 1021 DSIFYISVVAYFCLIFLMNLSMFCTVLVQLNSVKSQIQKTRRKMLHDLKGTMSLTFLLG 1080

Qy 1081 LTWGFAFFAWGPMRNFFLYLFAIFNTLQGFFIFVHFCVMKESVREQWQIHLCCGWLRLDN 1140
 |||||
 Db 1081 LTWGFAFFAWGPMRNFFLYLFAIFNTLQGFFIFVHFCVMKESVREQWQIHLCCGWLRLDN 1140

Qy 1141 SSDGSSRCQIKVGKQEGGLKKIFEHLLTPSLKSTATSSTFKSLGSAQGTPEISFPNDD 1200
 |||||
 Db 1141 SSDGSSRCQIKVGKQEGGLKKIFEHLLTPSLKSTATSSTFKSLGSAQGTPEISFPNDD 1200

Qy 1201 FDKDPYCSP 1210
 |||||
 Db 1201 FDKDPYCSP 1210

Result No.	Score	Query Match	Length	DB	ID	Description
1	604	9.7	1231	2	T18390	latrophilin-3, spl
2	604	9.7	1299	2	T18398	latrophilin-3, spl
3	599.5	9.6	1240	2	T18393	latrophilin-3, spl
4	599.5	9.6	1308	2	T18408	latrophilin-3, spl
5	599	9.6	1274	2	T18391	latrophilin-3, spl
6	599	9.6	1342	2	T18405	latrophilin-3, spl
7	599	9.6	1503	2	T18389	latrophilin-3, spl
8	599	9.6	1571	2	T18395	latrophilin-3, spl
9	594.5	9.5	1283	2	T18394	latrophilin-3, spl
10	594.5	9.5	1351	2	T18409	latrophilin-3, spl
11	594.5	9.5	1512	2	T18392	latrophilin-3, spl
12	594.5	9.5	1580	2	T18407	latrophilin-3, spl
13	591	9.5	1230	2	T17187	CL3AB protein - ra
14	591	9.5	1298	2	T17199	CL3BB protein - ra
15	586.5	9.4	1459	2	T17186	CL3AA protein - ra
16	586.5	9.4	1527	2	T17198	CL3BA protein - ra
17	586	9.4	1273	2	T17188	CL3AC protein - ra
18	586	9.4	1341	2	T18301	latrophilin-2, spl
19	586	9.4	1341	2	T17200	CL3BC protein - ra
20	586	9.4	1407	2	T18381	latrophilin-2 (spl

Result No.	Score	Query Match	Length	DB	ID	Description
1	495.5	7.9	1522	1	BAI3_HUMAN	O60242 homo sapien
2	481	7.7	931	1	EMR1_MOUSE	Q61549 mus musculu
3	457.5	7.3	1584	1	BAI1_HUMAN	O14514 homo sapien
4	457	7.3	886	1	EMR1_HUMAN	Q14246 homo sapien
5	437	7.0	1572	1	BAI2_HUMAN	O60241 homo sapien
6	425	6.8	835	1	CD97_HUMAN	P48960 homo sapien
7	419.5	6.7	3034	1	CLR1_MOUSE	O35161 mus musculu
8	416	6.7	2144	1	CLR2_RAT	Q9qyp2 rattus norv
9	414.5	6.6	3014	1	CLR1_HUMAN	Q9nyq6 homo sapien
10	409.5	6.6	2923	1	CLR2_HUMAN	Q9hcu4 homo sapien
11	409	6.6	2920	1	CLR2_MOUSE	Q9r0m0 mus musculu
12	325	5.2	3312	1	CLR3_HUMAN	Q9nyq7 homo sapien
13	318.5	5.1	3313	1	CLR3_RAT	O88278 rattus norv
14	318	5.1	3301	1	CLR3_MOUSE	Q91zi0 mus musculu
15	298	4.8	1367	1	AMYH_YEAST	P08640 saccharomyc

Result No.	Score	Query Match	Length	DB	ID	Description
1	4796.5	76.9	2799	4	Q8IZF6	Q8izf6 homo sapien
2	1313.5	21.1	1009	11	Q8CJ12	Q8cj12 mus musculu
3	1313.5	21.1	1014	4	O00406	O00406 homo sapien
4	1308	21.0	1006	11	Q8CJ09	Q8cj09 mus musculu
5	1307.5	21.0	995	11	Q8BL10	Q8bl10 mus musculu
6	1307	21.0	982	11	Q8CJ08	Q8cj08 mus musculu
7	1306.5	20.9	993	11	Q8CJ10	Q8cj10 mus musculu
8	1305	20.9	1003	4	Q8IZE6	Q8ize6 homo sapien
9	1304.5	20.9	1013	11	Q8CJ11	Q8cj11 rattus norv
10	1302	20.9	1017	4	Q8IZP9	Q8izp9 homo sapien
11	1300.5	20.8	985	11	Q8CJ06	Q8cj06 rattus norv
12	1300.5	20.8	997	11	Q8CJ07	Q8cj07 rattus norv
13	1299	20.8	987	4	Q8IZP4	Q8izp4 homo sapien
14	1299	20.8	1001	4	Q8IZE5	Q8ize5 homo sapien
15	1296	20.8	995	4	Q8IZP3	Q8izp3 homo sapien
16	1295.5	20.8	979	4	Q8IZE7	Q8ize7 homo sapien

Result No.	Score	Query Match	Length	DB	ID	Description
1	4796.5	76.9	2799	4	Q8IZF6	Q8izf6 homo sapien
2	1313.5	21.1	1009	11	Q8CJ12	Q8cj12 mus musculu
3	1313.5	21.1	1014	4	O00406	O00406 homo sapien
4	1308	21.0	1006	11	Q8CJ09	Q8cj09 mus musculu
5	1307.5	21.0	995	11	Q8BL10	Q8bl10 mus musculu
6	1307	21.0	982	11	Q8CJ08	Q8cj08 mus musculu
7	1306.5	20.9	993	11	Q8CJ10	Q8cj10 mus musculu
8	1305	20.9	1003	4	Q8IZE6	Q8ize6 homo sapien
9	1304.5	20.9	1013	11	Q8CJ11	Q8cj11 rattus norv
10	1302	20.9	1017	4	Q8IZP9	Q8izp9 homo sapien
11	1300.5	20.8	985	11	Q8CJ06	Q8cj06 rattus norv
12	1300.5	20.8	997	11	Q8CJ07	Q8cj07 rattus norv
13	1299	20.8	987	4	Q8IZP4	Q8izp4 homo sapien
14	1299	20.8	1001	4	Q8IZE5	Q8ize5 homo sapien
15	1296	20.8	995	4	Q8IZP3	Q8izp3 homo sapien
16	1295.5	20.8	979	4	Q8IZE7	Q8ize7 homo sapien

SEQ ID NO : 4

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	3852	100.0	733	5	AAU98552	Aau98552 Novel hum
2	3841.5	99.7	1210	5	AAU98551	Aau98551 Novel hum
3	3791	98.4	735	7	ADE34400	Ade34400 Human G-p
4	3791	98.4	1211	6	ABR61471	Abr61471 Human sec
5	3299	85.6	662	5	AAU98554	Aau98554 Novel hum
6	3299	85.6	1138	5	AAU98553	Aau98553 Novel hum
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8	2509	65.1	486	5	ABP52435	Abp52435 Human G p
9	1957.5	50.8	395	6	ABR61470	Abr61470 Human sec
10	1298	33.7	717	5	AAU99588	Aau99588 Human G p
11	1295.5	33.6	967	7	ADB80452	Adb80452 Ovarian c
12	1295.5	33.6	993	7	ADB80450	Adb80450 Ovarian c
13	1295.5	33.6	1000	7	ADB80458	Adb80458 Ovarian c
14	1295.5	33.6	1013	3	AAB01247	Aab01247 Human HE6
15	1295.5	33.6	1014	6	ABJ38840	Abj38840 Human G-p
16	1295.5	33.6	1014	6	ABJ38832	Abj38832 Human epi
17	1295.5	33.6	1014	6	ABP81971	Abp81971 Human G p
18	1295.5	33.6	1014	6	ABR61472	Abr61472 Human sec
19	1295.5	33.6	1014	7	ADB80456	Adb80456 Ovarian c

RESULT 1

AAU98552

ID AAU98552 standard; protein; 733 AA.

XX

AC AAU98552;

XX

DT 26-AUG-2002 (first entry)

XX

DE Novel human GPCR, 7TM protein #2.

XX

KW Human; G protein-coupled receptor; GPCR; 7TM protein;

KW physiological disorder; behavioural disorder; cosmetic; nutraceutical;

KW seven transmembrane protein; receptor.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Misc-difference 79

FT /note= "Encoded by AGATTC"

FT Misc-difference 724

FT /note= "Encoded by YTT"

XX

PN WO200236633-A2.

XX

PD 10-MAY-2002.

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PF 29-OCT-2001; 2001WO-US050938.

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PR 30-OCT-2000; 2000US-0244285P.

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PA (LEXI-) LEXICON GENETICS INC.

XX

PI Hu Y, Zambrowicz B, Nepomnichy B;

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DR WPI; 2002-490002/52.

DR N-PSDB; ABK85472.

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PT New human G protein-coupled receptor polynucleotide useful for

PT therapeutic, diagnostic and pharmacogenomic applications, and for

PT identifying compounds that modulate gene expression or gene product

PT activity.

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PS Claim 4; Page 77-78; 86pp; English.

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CC The present invention relates to novel human G protein-coupled receptor

CC (GPCR) proteins referred to as 7TM proteins, and the polynucleotide

CC sequences encoding them. The novel 7TM proteins have multiple

CC transmembrane regions. The polynucleotide and polypeptide sequences of

CC the invention can be used in the treatment of physiological or

CC behavioural disorders, and/or in cosmetic or nutraceutical applications.

CC The present sequence represents a human 7TM protein of the invention

XX

SQ Sequence 733 AA;

Query Match 100.0%; Score 3852; DB 5; Length 733;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 733; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRKIKSKIHGNTFGNFTQDQLTLLVNCEHVAVKKLEPGNCKADETASKYKGTWKLLTN 60

Db 1 MRKIKSKIHGNTFGNFTQDQLTLLVNCEHVAVKKLEPGNCKADETASKYKGTWKLLTN 60

QY 61 PTETAQTRCIKNEDGNATRCISISINTGKSQWEKPKFKQCKLLQELPKIVDLANITISDE 120

Db 61 PTETAQTRCIKNEDGNATRCISISINTGKSQWEKPKFKQCKLLQELPKIVDLANITISDE 120

QY 121 NPEDVAEHILNLINEPALGKEETKIIVSKISDISQCDEISMNLTHVMLQIINVVLEKQN 180

Db	121	NPEDVAEHILNLINEPALGKEETKIIVSKISDISQCDEISMNLTHVMLQIINVVLEKQN	180
Qy	181	NSASDLHEISNEILRIIERPGHKMEFSGQIANLAVAGLALAVLRGDHTFDGMAFSIHSYE	240
Db	181	NSASDLHEISNEILRIIERPGHKMEFSGQIANLAVAGLALAVLRGDHTFDGMAFSIHSYE	240
Qy	241	EGPDPDIFLGNVPVGGILASIYLPKSLTERIPLSNLQPILFNFFGQTSLEFKTKNVTKALT	300
Db	241	EGPDPDIFLGNVPVGGILASIYLPKSLTERIPLSNLQPILFNFFGQTSLEFKTKNVTKALT	300
Qy	301	TYVVSASISDMFIQNLADPVVITLQHIGGNQNYGQVHCAFWDFENNNGLGGWNSSGCKVK	360
Db	301	TYVVSASISDMFIQNLADPVVITLQHIGGNQNYGQVHCAFWDFENNNGLGGWNSSGCKVK	360
Qy	361	ETNVNYTICQCDHLTHFGVLMDSLRSSTVDSVNEQILALITYTGCGISSIFLGVAVVITYIA	420
Db	361	ETNVNYTICQCDHLTHFGVLMDSLRSSTVDSVNEQILALITYTGCGISSIFLGVAVVITYIA	420
Qy	421	FHKLRKDYPAKILINLCTALLMLNLVFLINSWLSSFQKVGVCITAAVALHYFLLVSTW	480
Db	421	FHKLRKDYPAKILINLCTALLMLNLVFLINSWLSSFQKVGVCITAAVALHYFLLVSTW	480
Qy	481	GLEAVHMYLALVKVFNIIYIPNYILKFCLVGWGIPAIMVAITVSVKKDLYGTLSP	540
Db	481	GLEAVHMYLALVKVFNIIYIPNYILKFCLVGWGIPAIMVAITVSVKKDLYGTLSP	540
Qy	541	IKDDSIIFYISVVAYFCLIFLMNLSMFCTVLVQLNSVKSQIQKTRRKMIHDLKGTMSLTF	600
Db	541	IKDDSIIFYISVVAYFCLIFLMNLSMFCTVLVQLNSVKSQIQKTRRKMIHDLKGTMSLTF	600
Qy	601	LLGLTWGFAFFAWGPMRNFLLYLFAIFNTLQGGFFIFVFHFCVMKESVREQWQIHLCCGWLR	660
Db	601	LLGLTWGFAFFAWGPMRNFLLYLFAIFNTLQGGFFIFVFHFCVMKESVREQWQIHLCCGWLR	660
Qy	661	LDNSSDGSSRCQIKVGKQEGGLKKIFEHKLTPSLKSTATSSTFKSLGSAQGTPSEISFP	720
Db	661	LDNSSDGSSRCQIKVGKQEGGLKKIFEHKLTPSLKSTATSSTFKSLGSAQGTPSEISFP	720
Qy	721	NDDFDKDPYCSP	733
Db	721	NDDFDKDPYCSP	733

Result No.	Score	Query Match Length	DB	ID	Description
1	585.5	15.2	1231	2 T18390	latrophilin-3, spl
2	585.5	15.2	1299	2 T18398	latrophilin-3, spl
3	582.5	15.1	1230	2 T17187	CL3AB protein - ra
4	582.5	15.1	1298	2 T17199	CL3BB protein - ra
5	581	15.1	1240	2 T18393	latrophilin-3, spl
6	581	15.1	1308	2 T18408	latrophilin-3, spl
7	580.5	15.1	1274	2 T18391	latrophilin-3, spl
8	580.5	15.1	1342	2 T18405	latrophilin-3, spl
9	580.5	15.1	1503	2 T18389	latrophilin-3, spl
10	580.5	15.1	1571	2 T18395	latrophilin-3, spl
11	578	15.0	1459	2 T17186	CL3AA protein - ra
12	578	15.0	1527	2 T17198	CL3BA protein - ra
13	577.5	15.0	1273	2 T17188	CL3AC protein - ra
14	577.5	15.0	1341	2 T18301	latrophilin-2, spl
15	577.5	15.0	1341	2 T17200	CL3BC protein - ra

Result No.	Score	Query Match Length	DB	ID	Description
1	488	12.7	1522	1 BAI3_HUMAN	O60242 homo sapien
2	466	12.1	931	1 EMR1_MOUSE	Q61549 mus musculu
3	457.5	11.9	886	1 EMR1_HUMAN	Q14246 homo sapien

4	450	11.7	1584	1	BAI1_HUMAN	O14514 homo sapien
5	429.5	11.2	1572	1	BAI2_HUMAN	O60241 homo sapien
6	425	11.0	835	1	CD97_HUMAN	P48960 homo sapien
7	416	10.8	2144	1	CLR2_RAT	Q9qyp2 rattus norv
8	412.5	10.7	3034	1	CLR1_MOUSE	O35161 mus musculu
9	409.5	10.6	2923	1	CLR2_HUMAN	Q9hcu4 homo sapien
10	409	10.6	2920	1	CLR2_MOUSE	Q9r0m0 mus musculu
11	405	10.5	3014	1	CLR1_HUMAN	Q9nyq6 homo sapien
12	325	8.4	3312	1	CLR3_HUMAN	Q9nyq7 homo sapien
13	318.5	8.3	3313	1	CLR3_RAT	O88278 rattus norv
14	318	8.3	3301	1	CLR3_MOUSE	Q91zi0 mus musculu
15	232.5	6.0	420	1	CRF1_CHICK	Q90812 gallus gall

Result No.	Score	% Match	Query Length	DB	ID	Description
1	3008.5	78.1	2799	4	Q8IZF6	Q8izf6 homo sapien
2	1300.5	33.8	985	11	Q8CJ06	Q8cj06 rattus norv
3	1300.5	33.8	997	11	Q8CJ07	Q8cj07 rattus norv
4	1300.5	33.8	1013	11	Q8CJ11	Q8cj11 rattus norv
5	1298.5	33.7	982	11	Q8CJ08	Q8cj08 mus musculu
6	1298.5	33.7	993	11	Q8CJ10	Q8cj10 mus musculu
7	1298.5	33.7	1006	11	Q8CJ09	Q8cj09 mus musculu
8	1298.5	33.7	1009	11	Q8CJ12	Q8cj12 mus musculu
9	1297.5	33.7	995	11	Q8BL10	Q8bl10 mus musculu
10	1295.5	33.6	979	4	Q8IZE7	Q8ize7 homo sapien
11	1295.5	33.6	987	4	Q8IZP4	Q8izp4 homo sapien
12	1295.5	33.6	993	4	Q8IZE4	Q8ize4 homo sapien
13	1295.5	33.6	995	4	Q8IZP3	Q8izp3 homo sapien
14	1295.5	33.6	1001	4	Q8IZE5	Q8ize5 homo sapien
15	1295.5	33.6	1003	4	Q8IZE6	Q8ize6 homo sapien

SEQ ID NO : 1

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	3632.6	100.0	3633	6	AX578154	AX578154 Sequence
2	3632.6	100.0	4185	6	AX578162	AX578162 Sequence
3	3326.8	91.6	3416	6	AX578158	AX578158 Sequence
4	2204.6	60.7	2205	6	AX578156	AX578156 Sequence
5	2169.2	59.7	8400	9	AY140954	AY140954 Homo sapi
6	1898.8	52.3	1988	6	AX578160	AX578160 Sequence
7	1314.2	36.2	1458	6	BD173766	BD173766 Novel G p
8	1120.8	30.9	63946	9	AL136167	AL136167 Human DNA
9	1120.8	30.9	204922	2	AL670274	AL670274 Homo sapi

RESULT 1

AX578154

LOCUS AX578154 3633 bp DNA linear PAT 08-JAN-2003

DEFINITION Sequence 1 from Patent WO0236633.

ACCESSION AX578154

VERSION AX578154.1 GI:27647360

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 Hu, Y., Zambrowicz, B. and Nepomnichy, B.

TITLE Novel human 7tm proteins and polynucleotides encoding the same

JOURNAL Patent: WO 0236633-A 1 10-MAY-2002;

Lexicon Genetics Incorporated (US)

FEATURES Location/Qualifiers
 source 1. .3633
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

ORIGIN

Query Match 100.0%; Score 3632.6; DB 6; Length 3633;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 3633; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGACATCTAGTAATACCCAACCTCTGCTTATGACTTCCTGGAACATACCCACAGCTGAA 60
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 Db 1 ATGACATCTAGTAATACCCAACCTCTGCTTATGACTTCCTGGAACATACCCACAGCTGAA 60

 Qy 61 GGTTCCTCAGTTTCCAATTTCCACCACTATTAATGTACCTACATCCAATGAGATGGAAACA 120
 |||
 Db 61 GGTTCCTCAGTTTCCAATTTCCACCACTATTAATGTACCTACATCCAATGAGATGGAAACA 120

 Qy 121 GAGACTCTACACCTTGTTTCCTGGGCCTTTGTCAACATTCACAGCCTCTCAGACTGGTCTA 180

RESULT 2

AX578162

LOCUS AX578162 4185 bp DNA linear PAT 08-JAN-2003

DEFINITION Sequence 9 from Patent WO0236633.

ACCESSION AX578162

VERSION AX578162.1 GI:27647364

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Hu,Y., Zambrowicz,B. and Nepomnichy,B.

TITLE Novel human 7tm proteins and polynucleotides encoding the same

JOURNAL Patent: WO 0236633-A 9 10-MAY-2002;

Lexicon Genetics Incorporated (US)

FEATURES Location/Qualifiers

 source 1. .4185
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

ORIGIN

Query Match 100.0%; Score 3632.6; DB 6; Length 4185;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 3633; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGACATCTAGTAATACCCAACCTCTGCTTATGACTTCCTGGAACATACCCACAGCTGAA 60
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 Db 472 ATGACATCTAGTAATACCCAACCTCTGCTTATGACTTCCTGGAACATACCCACAGCTGAA 531

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	3632.6	100.0	3633	6	ABK85471	Abk85471 DNA encod
2	3632.6	100.0	4185	6	ABK85475	Abk85475 ORF and f
3	3326.8	91.6	3416	6	ABK85473	Abk85473 DNA encod
4	2308.8	63.6	2486	9	ADE34398	Ade34398 Human G-p
5	2204.6	60.7	2205	6	ABK85472	Abk85472 DNA encod
6	2178.8	60.0	2208	9	ADE34399	Ade34399 Human G-p
7	1947	53.6	4161	7	ABQ76895	Abq76895 Human G-p

RESULT 1

ABK85471

ID ABK85471 standard; DNA; 3633 BP.

XX

AC ABK85471;
 XX
 DT 26-AUG-2002 (first entry)
 XX
 DE DNA encoding novel human GPCR, 7TM protein #1.
 XX
 KW Human; G protein-coupled receptor; GPCR; 7TM protein;
 KW physiological disorder; behavioural disorder; cosmetic; nutraceutical;
 KW seven transmembrane protein; gene; ds.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 1. .3633
 FT /*tag= a
 FT /product= "7TM protein #1"
 FT unsure 3601. .3603
 FT /*tag= b
 FT /note= "Encodes Phe"
 XX
 PN WO200236633-A2.
 XX
 PD 10-MAY-2002.
 XX
 PF 29-OCT-2001; 2001WO-US050938.
 XX
 PR 30-OCT-2000; 2000US-0244285P.
 XX
 PA (LEXI-) LEXICON GENETICS INC.
 XX
 PI Hu Y, Zambrowicz B, Nepomnichy B;
 XX
 DR WPI; 2002-490002/52.
 DR P-PSDB; AAU98551.
 XX
 PT New human G protein-coupled receptor polynucleotide useful for
 PT therapeutic, diagnostic and pharmacogenomic applications, and for
 PT identifying compounds that modulate gene expression or gene product
 PT activity.
 XX
 PS Claim 1; Page 72-73; 86pp; English.
 XX
 CC The present invention relates to novel human G protein-coupled receptor
 CC (GPCR) proteins referred to as 7TM proteins, and the polynucleotide
 CC sequences encoding them. The novel 7TM proteins have multiple
 CC transmembrane regions. The polynucleotide and polypeptide sequences of
 CC the invention can be used in the treatment of physiological or
 CC behavioural disorders, and/or in cosmetic or nutraceutical applications.
 CC The present sequence encodes a human 7TM protein of the invention
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 SQ Sequence 3633 BP; 1039 A; 840 C; 683 G; 1070 T; 0 U; 1 Other;

 Query Match 100.0%; Score 3632.6; DB 6; Length 3633;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 3633; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 1 ATGACATCTAGTAATACCCAACCTCTGCTTATGACTTCCTGGAACATACCCACAGCTGAA 60
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 Db 1 ATGACATCTAGTAATACCCAACCTCTGCTTATGACTTCCTGGAACATACCCACAGCTGAA 60

RESULT 2
 ABK85475
 ID ABK85475 standard; DNA; 4185 BP.
 XX
 AC ABK85475;
 XX
 DT 26-AUG-2002 (first entry)
 XX
 DE ORF and flanking regions for a novel human GPCR.
 XX

KW Human; G protein-coupled receptor; GPCR; 7TM protein;
 KW physiological disorder; behavioural disorder; cosmetic; nutraceutical;
 KW seven transmembrane protein; gene; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200236633-A2.
 XX
 PD 10-MAY-2002.
 XX
 PF 29-OCT-2001; 2001WO-US050938.
 XX
 PR 30-OCT-2000; 2000US-0244285P.
 XX
 PA (LEXI-) LEXICON GENETICS INC.
 XX
 PI Hu Y, Zambrowicz B, Nepomnichy B;
 XX
 DR WPI; 2002-490002/52.
 XX
 PT New human G protein-coupled receptor polynucleotide useful for
 PT therapeutic, diagnostic and pharmacogenomic applications, and for
 PT identifying compounds that modulate gene expression or gene product
 PT activity.
 XX
 PS Disclosure; Page 85-86; 86pp; English.
 XX
 CC The present invention relates to novel human G protein-coupled receptor
 CC (GPCR) proteins referred to as 7TM proteins, and the polynucleotide
 CC sequences encoding them. The novel 7TM proteins have multiple
 CC transmembrane regions. The polynucleotide and polypeptide sequences of
 CC the invention can be used in the treatment of physiological or
 CC behavioural disorders, and/or in cosmetic or nutraceutical applications.
 CC The present sequence represents an ORF and the flanking regions for a
 CC novel human GPCR
 XX
 SQ Sequence 4185 BP; 1211 A; 974 C; 763 G; 1235 T; 0 U; 2 Other;

Query Match 100.0%; Score 3632.6; DB 6; Length 4185;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 3633; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGACATCTAGTAATACCCAACCTCTGCTTATGACTTCCTGGAACATACCCACAGCTGAA 60
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 Db 472 ATGACATCTAGTAATACCCAACCTCTGCTTATGACTTCCTGGAACATACCCACAGCTGAA 531

SEQ ID NO: 3

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	2204.6	100.0	2205	6	AX578156	AX578156 Sequence
2	2204.6	100.0	3633	6	AX578154	AX578154 Sequence
3	2204.6	100.0	4185	6	AX578162	AX578162 Sequence
4	1898.8	86.1	1988	6	AX578160	AX578160 Sequence
5	1898.8	86.1	3416	6	AX578158	AX578158 Sequence
6	1478.2	67.0	8400	9	AY140954	AY140954 Homo sapi
7	1314.2	59.6	1458	6	BD173766	BD173766 Novel G p
8	1089	49.4	1185	6	AX794833	AX794833 Sequence
9	355.6	16.1	4651	9	AY143364	AY143364 Homo sapi
10	355.6	16.1	4665	6	A93546	A93546 Sequence 1
11	355.6	16.1	4665	6	AX549142	AX549142 Sequence

RESULT 1
 AX578156

LOCUS AX578156 2205 bp DNA linear PAT 08-JAN-2003
 DEFINITION Sequence 3 from Patent WO0236633.
 ACCESSION AX578156
 VERSION AX578156.1 GI:27647361
 KEYWORDS .
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Hu,Y., Zambrowicz,B. and Nepomnichy,B.
 TITLE Novel human 7tm proteins and polynucleotides encoding the same
 JOURNAL Patent: WO 0236633-A 3 10-MAY-2002;
 Lexicon Genetics Incorporated (US)
 FEATURES Location/Qualifiers
 source 1. .2205
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

ORIGIN

Query Match 100.0%; Score 2204.6; DB 6; Length 2205;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2205; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAGAAAATCAAAAGTAAAATACATGGCAACTTCACACATGGAACTTCACACAAGAT 60
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 Db 1 ATGAGAAAATCAAAAGTAAAATACATGGCAACTTCACACATGGAACTTCACACAAGAT 60

RESULT 2

AX578154
 LOCUS AX578154 3633 bp DNA linear PAT 08-JAN-2003
 DEFINITION Sequence 1 from Patent WO0236633.
 ACCESSION AX578154
 VERSION AX578154.1 GI:27647360
 KEYWORDS .
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Hu,Y., Zambrowicz,B. and Nepomnichy,B.
 TITLE Novel human 7tm proteins and polynucleotides encoding the same
 JOURNAL Patent: WO 0236633-A 1 10-MAY-2002;
 Lexicon Genetics Incorporated (US)
 FEATURES Location/Qualifiers
 source 1. .3633
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

ORIGIN

Query Match 100.0%; Score 2204.6; DB 6; Length 3633;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2205; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAGAAAATCAAAAGTAAAATACATGGCAACTTCACACATGGAACTTCACACAAGAT 60
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 Db 1429 ATGAGAAAATCAAAAGTAAAATACATGGCAACTTCACACATGGAACTTCACACAAGAT 1488

RESULT 3

AX578162
 LOCUS AX578162 4185 bp DNA linear PAT 08-JAN-2003
 DEFINITION Sequence 9 from Patent WO0236633.
 ACCESSION AX578162
 VERSION AX578162.1 GI:27647364
 KEYWORDS .

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Hu,Y., Zambrowicz,B. and Nepomnichy,B.
 TITLE Novel human 7tm proteins and polynucleotides encoding the same
 JOURNAL Patent: WO 0236633-A 9 10-MAY-2002;
 Lexicon Genetics Incorporated (US)
 FEATURES Location/Qualifiers
 source 1..4185
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

ORIGIN

Query Match 100.0%; Score 2204.6; DB 6; Length 4185;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2205; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAGAAAAATCAAAAGTAAAATACATGGCAACTTCACACATGGAAACTTCACACAAGAT 60
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 Db 1900 ATGAGAAAAATCAAAAGTAAAATACATGGCAACTTCACACATGGAAACTTCACACAAGAT 1959
 Qy 61 CAATTGACGTTATTAGTAAACTGTGAACACGTTGCAGTGAAAAAACTAGAGCCTGGAAAT 120
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 Db 1960 CAATTGACGTTATTAGTAAACTGTGAACACGTTGCAGTGAAAAAACTAGAGCCTGGAAAT 2019